

L3 ANSWER 10 OF 10 MEDLINE DUPLICATE 10  
ACCESSION NUMBER: 96006701 MEDLINE  
DOCUMENT NUMBER: 96006701 PubMed ID: 7550366  
TITLE: Polymorphisms of human Ah receptor gene are not involved  
in  
lung cancer.  
AUTHOR: Kawajiri K; Watanabe J; Eguchi H; Nakachi K; Kiyohara C;  
Hayashi S  
CORPORATE SOURCE: Department of Biochemistry, Saitama Cancer Center Research  
Institute, Japan.  
SOURCE: PHARMACOGENETICS, (1995 Jun) 5 (3) 151-8.  
Journal code: 9211735. ISSN: 0960-314X.  
PUB. COUNTRY: ENGLAND: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199510  
ENTRY DATE: Entered STN: 19951227  
Last Updated on STN: 19970203  
Entered Medline: 19951024  
AB The Ah receptor (Ahr) is a ligand-dependent transcription factor that  
positively regulates inducible expression of the CYP1A1 gene. Based on  
the  
sequence information of the human Ahr and the intron-exon  
junctions of the mouse counterpart, an analysis of single-strand  
conformational polymorphism (SSCP) was carried out to detect subtle base  
differences in the coding region of the gene among individuals. We found  
that the Ahr protein has at least two forms of variants in a Japanese  
gene  
pool, and that these variants can be ascribed to one amino acid  
replacement of Arg by Lys at codon 554. The frequencies of Arg-coded and  
Lys-coded alleles were 0.57 and 0.43, respectively. We found, however,  
that this germ line polymorphism of the Ahr gene did not show a  
significant association with aryl hydrocarbon hydroxylase (**AHH**)  
inducibility nor with lung cancer incidence.

L3 ANSWER 8 OF 10 MEDLINE DUPLICATE 8

ACCESSION NUMBER: 96439142 MEDLINE

DOCUMENT NUMBER: 96439142 PubMed ID: 8841477

TITLE: A mutation in the p53 tumor suppressor gene of **AHH**-1 tk+/- human lymphoblastoid cells.

AUTHOR: Morris S M; Manjanatha M G; Shelton S D; Domon O E; McGarrity L J; Casciano D A

CORPORATE SOURCE: Division of Genetic Toxicology, Food and Drug Administration, Department of Health and Human Services, Jefferson, AR 72079, USA.. smorris@nctr.fda.gov

SOURCE: MUTATION RESEARCH, (1996 Sep 23) 356 (2) 129-34.  
Journal code: 0400763. ISSN: 0027-5107.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199611

ENTRY DATE: Entered STN: 19961219  
Last Updated on STN: 19961219  
Entered Medline: 19961120

AB Loss-of-function mutations in the p53 tumor suppressor gene result in an altered response to DNA-damaging agents. Included in the mutant p53 phenotype are the loss of the G1 checkpoint and delayed apoptotic cell death, characteristics we have consistently observed in the **AHH**-1 tk+/- cell line following exposure to DNA-damaging agents. In order to determine the functional status of p53 in the **AHH**-1 tk+/- cell line, molecular analysis (single-strand conformational polymorphism [SSCP]) and sequence analysis) was performed on exons 5-9 of the p53 gene. In addition, the status of the p53 gene in the closely related lymphoblast line, MCL-5, which, in our hands, has a much higher spontaneous rate of apoptosis than **AHH**-1 tk+/-, was also determined by molecular analysis. Initial SSCP analysis of **AHH**-1 tk+/- revealed an abnormal migration pattern of exon 8 when compared to a wild-type control. Subsequent sequence analysis indicated that a base-pair substitution (CGG-->TGG) mutation had occurred at codon 282, a reported "hot spot" for 5-methylcytosine mutations in the human p53 gene. Neither SSCP nor sequence analysis of exons 5-9 of MCL-5 indicated any differences from wild-type DNA. These results suggest that the lack of a G1 arrest and the delayed entrance into apoptosis observed in chemically-exposed **AHH**-1 tk+/- cells are, at least partially, accounted for by a loss-of-function mutation in the p53 gene.

L3 ANSWER 4 OF 10 MEDLINE DUPLICATE 4  
ACCESSION NUMBER: 2001106027 MEDLINE  
DOCUMENT NUMBER: 20564328 PubMed ID: 10956665  
TITLE: **Aspartyl beta -hydroxylase**  
(Asph) and an evolutionarily conserved isoform of Asph missing the catalytic domain share **exons** with junctin.  
AUTHOR: Dinchuk J E; Henderson N L; Burn T C; Huber R; Ho S P;  
Link  
CORPORATE SOURCE: J; O'Neil K T; Focht R J; Scully M S; Hollis J M; Hollis G  
Pharmaceuticals F; Friedman P A  
Department of Applied Biotechnology, DuPont  
Research Laboratories, DuPont Pharmaceuticals Company,  
Experimental Station, Wilmington, Delaware 19880, USA..  
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SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Dec 15) 275 (50)  
39543-54.  
Journal code: 2985121R. ISSN: 0021-9258.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-AF289199; GENBANK-AF289200; GENBANK-AF289205;  
GENBANK-AF289206; GENBANK-AF289207; GENBANK-AF289208;  
GENBANK-AF289209; GENBANK-AF289210; GENBANK-AF289211;  
GENBANK-AF289212; GENBANK-AF289213; GENBANK-AF289214;  
GENBANK-AF289215; GENBANK-AF289486; GENBANK-AF289487;  
GENBANK-AF289488; GENBANK-AF289489; GENBANK-AF289490;  
GENBANK-AF289491; GENBANK-AF289492; GENBANK-AF289493;  
GENBANK-AF289494  
ENTRY MONTH: 200102  
ENTRY DATE: Entered STN: 20010322  
Last Updated on STN: 20010322  
Entered Medline: 20010208  
AB The mouse **aspartyl beta-hydroxylase** gene (Asph, BAH) has been cloned and characterized. The mouse BAH gene spans 200 kilobase pairs of genomic DNA and contains 24 **exons**. Of three major BAH-related transcripts, the two largest (6,629 and 4,419 base pairs) encode full-length protein and differ only in the use of alternative polyadenylation signals. The smallest BAH-related transcript (2,789 base pairs) uses an alternative 3' terminal **exon**, resulting in a protein lacking a catalytic domain. Evolutionary conservation of this noncatalytic isoform of BAH (humbug) is demonstrated in mouse, man, and Drosophila. Monoclonal antibody reagents were generated, epitope-mapped, and used to definitively correlate RNA bands on Northern blots with protein species on Western blots. The gene for mouse junctin, a calsequestrin-binding protein, was cloned and characterized and shown to be encoded from the same locus. When expressed in heart tissue, BAH/humbug preferably use the first **exon** and often the fourth **exon** of junctin while preserving the reading frame. Thus, three individual genes share common **exons** and open reading frames and use separate promoters to achieve differential expression, splicing, and function in a variety of tissues. This unusual form of **exon** sharing suggests that the functions of junctin, BAH, and humbug may be linked.

L3 ANSWER 3 OF 10 MEDLINE DUPLICATE 3  
ACCESSION NUMBER: 2001106028 MEDLINE  
DOCUMENT NUMBER: 20564329 PubMed ID: 11007777  
TITLE: Molecular cloning, expression, functional  
characterization,  
chromosomal localization, and gene structure of junctate,  
a  
novel integral calcium binding protein of  
sarco(endo)plasmic reticulum membrane.  
AUTHOR: Treves S; Feriutto G; Moccagatta L; Gambari R; Zorzato F  
CORPORATE SOURCE: Departments of Anaesthesia and Research, Hebelstrasse 20,  
Kantonsspital, 4031 Basel, Switzerland.  
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Dec 15) 275 (50)  
39555-68.  
Journal code: 2985121R. ISSN: 0021-9258.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-AF306765  
ENTRY MONTH: 200102  
ENTRY DATE: Entered STN: 20010322  
Last Updated on STN: 20010322  
Entered Medline: 20010208  
AB Screening a cDNA library from human skeletal muscle and cardiac muscle  
with a cDNA probe derived from junctin led to the isolation of two groups  
of cDNA clones. The first group displayed a deduced amino acid sequence  
that is 84% identical to that of dog heart junctin, whereas the second  
group had a single open reading frame that encoded a polypeptide with a  
predicted mass of 33 kDa, whose first 78 NH<sub>2</sub>-terminal residues are  
identical to junctin whereas its COOH terminus domain is identical to  
**aspartyl beta-hydroxylase**, a member of the  
alpha-ketoglutarate-dependent dioxygenase family. We named the latter  
amino acid sequence junctate. Northern blot analysis indicates that  
junctate is expressed in a variety of human tissues including heart,  
pancreas, brain, lung, liver, kidney, and skeletal muscle. Fluorescence  
in situ hybridization analysis revealed that the genetic loci of junctin and  
junctate map to the same cytogenetic band on human chromosome 8. Analysis  
of intron/exon boundaries of the genomic BAC clones demonstrate  
that junctin, junctate, and **aspartyl beta-**  
**hydroxylase** result from alternative splicing of the same gene. The  
predicted luminal portion of junctate is enriched in negatively charged  
residues and is able to bind calcium. Scatchard analysis of equilibrium  
(45)Ca(2+) binding in the presence of a physiological concentration of  
KC1 demonstrate that junctate binds 21.0 mol of Ca(2+)/mol protein with a  
k(D) of 217 +/- 20 microm (n = 5). Tagging recombinant junctate with green  
fluorescent protein and expressing the chimeric polypeptide in  
COS-7-transfected cells indicates that junctate is located in endoplasmic  
reticulum membranes and that its presence increases the peak amplitude  
and transient calcium released by activation of surface membrane receptors  
coupled to InsP(3) receptor activation. Our study shows that alternative  
splicing of the same gene generates the following functionally distinct  
proteins: an enzyme (**aspartyl beta-hydroxylase**), a structural protein of SR (junctin), and a membrane-bound calcium  
binding protein (junctate).

L3 ANSWER 1 OF 10 MEDLINE DUPLICATE 1  
ACCESSION NUMBER: 2002204823 MEDLINE  
DOCUMENT NUMBER: 21935316 PubMed ID: 11773073  
TITLE: Absence of post-translational aspartyl beta-hydroxylation of epidermal growth factor domains in mice leads to developmental defects and an increased incidence of intestinal neoplasia.  
AUTHOR: Dinchuk Joseph E; Focht Richard J; Kelley Jennifer A; Henderson Nancy L; Zolotarjova Nina I; Wynn Richard; Neff Nicola T; Link John; Huber Reid M; Burn Timothy C; Rupar Mark J; Cunningham Mark R; Selling Bernard H; Ma Jianhong; Stern Andrew A; Hollis Gregory F; Stein Robert B; Friedman Paul A  
CORPORATE SOURCE: Bristol-Myers Squibb Pharma Research Labs, Inc.,  
Wilmington, DE 19880-0400, USA.. joseph.dinchuk@bms.com  
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Apr 12) 277 (15)  
12970-7.  
Journal code: 2985121R. ISSN: 0021-9258.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200205  
ENTRY DATE: Entered STN: 20020409  
Last Updated on STN: 20020517  
Entered Medline: 20020516  
AB The BAH genomic locus encodes three distinct proteins: junctin, humbug, and BAH. All three proteins share common **exons**, but differ significantly based upon the use of alternative terminal **exons**. The biological roles of BAH and humbug and their functional relationship to junctin remain unclear. To evaluate the role of BAH *in vivo*, the catalytic domain of BAH was specifically targeted such that the coding regions of junctin and humbug remained undisturbed. BAH null mice lack measurable BAH protein in several tissues, lack **aspartyl beta-hydroxylase** activity in liver preparations, and exhibit no hydroxylation of the epidermal growth factor (EGF) domain of clotting Factor X. In addition to reduced fertility in females, BAH null mice display several developmental defects including syndactyly, facial dysmorphology, and a mild defect in hard palate formation. The developmental defects present in BAH null mice are similar to defects observed in knock-outs and hypomorphs of the Notch ligand Serrate-2. In this work, beta-hydroxylation of Asp residues in EGF domains is demonstrated for a soluble form of a Notch ligand, human Jagged-1. These results along with recent reports that another post-translational modification of EGF domains in Notch gene family members (glycosylation by Fringe) alters Notch pathway signaling, lends credence to the suggestion that aspartyl beta-hydroxylation may represent another post-translational modification of EGF domains that can modulate Notch pathway signaling. Previous work has demonstrated increased levels of BAH in certain tumor tissues and a role for BAH in tumorigenesis has been proposed. The role of hydroxylase in tumor formation was tested directly by crossing BAH KO mice with an intestinal tumor model, APCmin mice. Surprisingly, BAH null/APCmin mice show a statistically significant increase in both intestinal polyp size and number when compared with BAH wild-type/APCmin controls. These results suggest that, in contrast to expectations, loss of BAH catalytic

activity may promote tumor formation.